REMARKS

Claims 1-20 were originally filed and were subject to a Restriction Requirement. Applicants affirm election, with traverse, of original claims 1-6, corresponding to the invention of Group I. The Examiner stated the he will examine all sequences, SEQ ID NOs:1-10 within the scope of Group I. Applicants thank the Examiner for his reconsideration of the Restriction Requirement. The specification has been amended to delete recitation of certain Web site designations. No new matter is added by any of these amendments, and entry of the amendments is requested.

Objection to the Disclosure

The Examiner has objected to the disclosure because it contains an embedded hyperlink and/or other form of browser-executable code (page 29, line 11) and that this is not permitted according to MPEP § 608.01.

Applicants submit that the MPEP states at § 608.01 that this policy is based on the principle that "USPTO policy does not permit the USPTO to link to any commercial sites since the USPTO exercises no control over the organization, views or accuracy of the information contained on those outside sites (underline added). Section 608.01 goes on to state that "where hyperlinks and/or other forms of browser-executable codes are a part of the applicant's invention and it is necessary to have them included in the patent application in order to comply with the requirements of 35 U.S.C. 112, first paragraph, and applicant does not intend to have these hyperlinks as active links, examiners should not object to these hyperlinks. The Office will disable these hyperlinks when preparing the text to be loaded onto the USPTO web database (underline added). Applicants point out that the cited website is a non-commercial, government web site which should not be subject to the requirements of MPEP § 608.01. However, this citation, as well as a second at page 30, line 21 have been deleted. Withdrawal of the objection is therefore requested.

Information Disclosure Statement

The Examiner stated that the information disclosure statement filed March 8, 2001 failss ssto comply with 37 CFR 1.98 (a)(1) which requires a list of all patents, publications, or other information submitted for consideration by the Office. The Examiner stated that it (the IDS) has been placed in the application file, but the information referred to therein has not been considered. In order for the references to be officially considered, PTO-1449 must be submitted.

An examination of Applicants application file record shows the PTO-1449 form was filed at the time of submission of the information disclosure statement as indicated by the return postcard, a copy of which is attached to this response. However, for the Examiner's convenience, a copy of the previously submitted PTO-1449 form is also attached.

35 U.S.C. § 102(a), Rejection of Claims 1, 2, 4, and 5

The Examiner has rejected claims 1, 2, 4, and 5 under 35 U.S.C. § 102(a) as being anticipated by Pallavicini et al. (GenBank Accession No. AJ304805, December 21, 2000). The Examiner stated that Pallavicini et al. teach a polynucleotide comprising a nucleic acid encoding the amino acid sequence of SEQ ID NO:1, a nucleic acid sequence which is 95.8 identical with SEQ ID NO:2. The Examiner stated further that Pallavicini et al. inherently teach a host cell comprising a vector containing the cDNA sequence, thereby meeting the limitations of claims 1, 2, 4 and 5 of the instant application.

In response to the rejection, applicants have filed a preliminary amendment to the instant application on August 1, 2002 for a claim to domestic priority under 35 U.S.C. § 120 to U.S. Application Serial No. 09/299,708, filed on April 26, 1999, now abandoned. Applicants submit that this application discloses SEQ ID NOs: 1 and 2 of the instant application prior to Pallavicini et al. and therefore that claims 1, 2, 4 and 5 of the instant application are not anticipated by Pallavicini et al. Applicants have furthermore filed a petition under 37 CFR § 1.78 to accept an unintentionally delayed priority claim to the above application on August 5, 2002, and respectfully request the Examiner to hold the present rejection in abeyance until a decision on this petition is received.

35 U.S.C. § 103(a), Rejection of Claims 3 and 6

The Examiner has rejected claims 3 and 6 under 35 U.S.C. § 103(a) as being unpatentable over Pallavicini et al. in view of Raju (U.S. Patent No. 6,261,818, filed April 14, 1999). The Examiner stated that the teachings of Pallavicini et al. are supra. The Examiner stated that Pallavicini et al. do not teach a labeling moiety in the composition of claim 3 or a method of using a host cell comprising a vector to produce a protein, as recited in claim 6. However, the Examiner stated, Raju teaches a cardiac-related ankyrin-repeat protein kinase, labelo group attached to the nucleotide sequence, and a method of producing the protein. The Examiner stated therefore that it would have been obvious to one of ordinary skill in the art at the time the instant application was filed to apply the teachings to Raju to the cDNA

taught by Pallavicini et al. to include a labeling group in the cDNA and to produce the protein encoded by the cDNA.

Applicants response to the rejection of claims under 35 U.S.C. § 102(a) as being anticipated by Pallavicini et al. have been discussed above. Raju does not teach or suggest a polynucleotide encoding SEQ ID NO:1 as recited in claim 1 and dependent claims 3 and 6. Applicants submit that for there to be a proper *prima facie* case of obviousness to a claim, the reference, or combination of references must teach or suggest all the claim limitations. Since Raju does not teach or suggest a polynucleotide encoding SEQ ID NO:1, Applicants submit that there is no proper prima facie case of obviousness against claims 3 or 6, and withdrawal of the rejection under 35 U.S.C. § 103(a) is therefore requested.

CONCLUSION

In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance, and request that the Examiner withdraw the outstanding objection and rejections. Early notice to that effect is earnestly solicited. Applicants further request that upon allowance of claims 1 and 3, that claims 7-12 be rejoined and examined as methods of use the the compositions of matter of claim 1 and 3 that depend from and are of the same scope as claims 1 and 3 in accordance with *Ochiai and Brouwer*. See MPEP § 821.04 and the Commissioner's Notice in the Official Gazette of March 26, 1996.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact Applicants' Agent of Record, below.

Please charge Deposit Account No. 09-0108 in the amount of $110.00 as set forth in the enclosed fee transmittal letter. If the USPTO determines that an additional fee is necessary, please charge any required fee to Deposit Account No. 09-0108.

Respectfully submitted,

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Version with markings to show changes made

IN THE SPECIFICATION:

Paragraph beginning at line10 of page 29 has been amended as follows:

The BLAST software suite, freely available sequence comparison algorithms (NCBI, Bethesda MD[; **http://www.ncbi.nlm.nih.gov/gorf/bl2.html**]), includes various sequence analysis programs including "blastn" that is used to align nucleic acid molecules and BLAST 2 that is used for direct pairwise comparison of either nucleic or amino acid molecules. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity is measured over the entire length of a sequence or some smaller portion thereof. Brenner et al. (1998; Proc Natl Acad Sci 95:6073-6078, incorporated herein by reference) analyzed the BLAST for its ability to identify structural homologs by sequence identity and found 30% identity is a reliable threshold for sequence alignments of at least 150 residues and 40%, for alignments of at least 70 residues.

Paragraph beginning at line15 of page 30 has been amended as follows:

Following assembly, templates were subjected to BLAST, motif, and other functional analyses and categorized in protein hierarchies using methods described in USSN 08/812,290 and USSN 08/811,758, both filed March 6, 1997; in USSN 08/947,845, filed October 9, 1997; and in USSN 09/034,807, filed March 4, 1998. Then templates were analyzed by translating each template in all three forward reading frames and searching each translation against the PFAM database of hidden Markov model-based protein families and domains using the HMMER software package (Washington University School of Medicine, St. Louis MO[; **http://pfam.wustl.edu/**]). The cDNA was further analyzed using MACDNASIS PRO software (Hitachi Software Engineering), and LASERGENE software (DNASTAR) and queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases, SwissProt, BLOCKS, PRINTS, PFAM, and Prosite.